

# SEQUENCE LISTING

<110> Houghton, Michael

<120> HCV FUSION PROTEINS WITH MODIFIED NS3 DOMAINS

<130> PP19545.003 (2300-19545)

<150> 60/394,510

<151> 2002-07-08

<150> 60/393,694

<151> 2002-07-02

<150> 09/721,479

<151> 2000-11-22

<150> 60/167,502

<151> 1999-11-24

<160> 8

<170> PatentIn version 3.2

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<212> PRT

<213> Artificial

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<223> epitope recognized by a Tcell receptor

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His Glu Tyr Pro Val Gly Ser Gln Leu

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<212> DNA

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<223> DNA sequence of a representative native, unmodified NS3 protease domain

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tgc ata atc acc agc cta act ggc cgg gac aaa aac caa gtg gag ggt 96
Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
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gag gtc cag att gtg tca act gct gcc caa acc ttc ctg gca acg tgc 144
Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala Thr Cys
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Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
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atc gcg tca ccc aag ggt cct gtc atc cag atg tat acc aat gta gac 240
Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp
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caa gac ctt gtg ggc tgg ccc gct ccg caa ggt agc cga tca ttg aca 288
Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr
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ccc tgc act tgc ggc tcc tcg gac ctt tac ctg gtc acg agg cac gcc 336
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
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gat gtc att ccc gtg cgc cgg cgg ggt gat agc agg ggc agc ctg ctg 384
Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
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tcg ccc cgg ccc att tcc tac ttg aaa ggc tcc tcg ggg ggt ccg ctg 432
Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
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ttg tgc ccc gcg ggg cac gcc gtg ggc ata ttt agg gcc gcg gtg tgc 480
Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
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acc cgt gga gtg gct aag gcg gtg gac ttt atc cct gtg gag aac cta 528
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu
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<211> 182  
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 <213> Artificial

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<400> 4

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Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala Thr Cys
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Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
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Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp
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Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr
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Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
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Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
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Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
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Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
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 <223> DNA sequence of a representative modified fusion protein, with  
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 amino acids 1-121 of Core on the C-terminus

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Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His	
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ggg atc gat cct aac atc agg acc ggg gtg aga aca att acc act ggc	144
Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly	
35 40 45	
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Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly	
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Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser	
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Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala	
85 90 95	
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Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro	
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Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser	
115 120 125	
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Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala	
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Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val	
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Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe	
195 200 205	
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210 215 220	

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Thr	Ala	Ile	Leu	Ser	Ser	Leu	Thr	Val	Thr	Gln	Leu	Leu	Arg	Arg	Leu	
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Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Gln Pro	
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gaa tac gac ttg gag ctc ata aca tca tgc tcc tcc aac gtg tca gtc	4656
Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser Asn Val Ser Val	
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gcc cac gac ggc gct gga aag agg gtc tac tac ctc acc cgt gac cct	4704
Ala His Asp Gly Ala Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro	
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aca acc ccc ctc gcg aga gct gcg tgg gag aca gca aga cac act cca	4752
Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr Pro	
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gtc aat tcc tgg cta ggc aac ata atc atg ttt gcc ccc aca ctg tgg	4800

Val 1585	Asn	Ser	Trp	Leu	Gly 1590	Asn	Ile	Ile	Met	Phe	Ala	Pro	Thr	Leu	Trp 1600	
gcg Ala	agg Arg	atg Met	ata Ile	ctg Leu	atg Met	acc Thr	cat His	ttc Phe	ttt Phe	agc Ser	gtc Val	ctt Leu	ata Ile	gcc Ala	agg Arg	4848
				1605					1610						1615	
gac Asp	cag Gln	ctt Leu	gaa Glu	cag Gln	gcc Ala	ctc Leu	gat Asp	tgc Cys	gag Glu	atc Ile	tac Tyr	ggg Gly	gcc Ala	tgc Cys	tac Tyr	4896
				1620				1625					1630			
tcc Ser	ata Ile	gaa Glu	cca Pro	ctg Leu	gat Asp	cta Leu	cct Pro	cca Pro	atc Ile	att Ile	caa Gln	aga Arg	ctc Leu	cat His	ggc Gly	4944
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ctc Leu	agc Ser	gca Ala	ttt Phe	tca Ser	ctc Leu	cac His	agt Ser	tac Tyr	tct Ser	cca Pro	ggg Gly	gaa Glu	atc Ile	aat Asn	agg Arg	4992
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aga Arg	cac His	cgg Arg	gcc Ala	cgg Arg	agc Ser	gtc Val	cgc Arg	gct Ala	agg Arg	ctt Leu	ctg Leu	gcc Ala	aga Arg	gga Gly	ggc Gly	5088
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agg Arg	gct Ala	gcc Ala	ata Ile	tgt Cys	ggc Gly	aag Lys	tac Tyr	ctc Leu	ttc Phe	aac Asn	tgg Trp	gca Ala	gta Val	aga Arg	aca Thr	5136
			1700					1705				1710				
aag Lys	ctc Leu	aaa Lys	ctc Leu	act Thr	cca Pro	ata Ile	gcg Ala	gcc Ala	gct Ala	ggc Gly	cag Gln	ctg Leu	gac Asp	ttg Leu	tcc Ser	5184
	1715						1720				1725					
ggc Gly	tgg Trp	ttc Phe	acg Thr	gct Ala	ggc Gly	tac Tyr	agc Ser	ggg Gly	gga Gly	gac Asp	att Ile	tat Tyr	cac His	agc Ser	gtg Val	5232
	1730					1735				1740						
tct Ser	cat His	gcc Ala	cgg Arg	ccc Pro	cgc Arg	tgg Trp	atc Ile	tgg Trp	ttt Phe	tgc Cys	cta Leu	ctc Leu	ctg Leu	ctt Leu	gct Ala	5280
1745					1750				1755						1760	
gca Ala	ggg Gly	gta Val	ggc Gly	atc Ile	tac Tyr	ctc Leu	ctc Leu	ccc Pro	aac Asn	cga Arg	atg Met	agc Ser	acg Thr	aat Asn	cct Pro	5328
				1765					1770					1775		
aaa Lys	cct Pro	caa Gln	aga Arg	aag Lys	acc Thr	aaa Lys	cgt Arg	aac Asn	acc Thr	aac Asn	cgg Arg	cgg Arg	ccg Pro	cag Gln	gac Asp	5376
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gtc Val	aag Lys	ttc Phe	ccg Pro	ggg Gly	ggc Gly	ggg Gly	cag Gln	atc Ile	gtt Val	ggt Gly	gga Gly	gtt Val	tac Tyr	ttg Leu	ttg Leu	5424
	1795						1800				1805					
ccg Pro	cgc Arg	agg Arg	ggc Gly	cct Pro	aga Arg	ttg Leu	ggg Gly	gtg Val	cgc Arg	gcg Ala	acg Thr	aga Arg	aag Lys	act Thr	tcc Ser	5472

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gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gct cgt			5520
Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg			
1825	1830	1835	1840
cgg ccc gag ggc agg acc tgg gct cag ccc ggg tac cct tgg ccc ctc			5568
Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu			
	1845	1850	1855
tat ggc aat gag ggc tgc ggg tgg gcg gga tgg ctc ctg tct ccc cgt			5616
Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg			
	1860	1865	1870
ggc tct cgg cct agc tgg ggc ccc aca gac ccc cgg cgt agg tcg cgc			5664
Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg			
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Asn Leu Gly Lys			
1890			

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 <213> Artificial

<220>  
 <223> amino acid sequence of a representative modified fusion protein,  
 with the NS3 protease domain deleted from the N-terminus and  
 including amino acids 1-121 of Core on the C-terminus

<400> 6

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Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly
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Ser	Pro	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly
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Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser
65					70					75					80
Thr	Asp	Ala	Thr	Ser	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala
				85					90					95	
Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro
		100						105					110		
Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser

115					120					125					
Thr	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Leu	Glu	Val
130					135					140					
Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys
145					150					155					160
Asp	Glu	Leu	Ala	Ala	Lys	Leu	Val	Ala	Leu	Gly	Ile	Asn	Ala	Val	Ala
				165					170					175	
Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	Thr	Ser	Gly	Asp	Val
			180					185					190		
Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe
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Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe
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Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Ile	Thr	Leu	Pro	Gln	Asp
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Ala	Val	Ser	Arg	Thr	Gln	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Lys	Pro
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Gly	Ile	Tyr	Arg	Phe	Val	Ala	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe
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Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr
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Glu	Leu	Thr	Pro	Ala	Glu	Thr	Thr	Val	Arg	Leu	Arg	Ala	Tyr	Met	Asn
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Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Gly
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Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr
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Lys	Gln	Ser	Gly	Glu	Asn	Leu	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr
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Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp
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Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu
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Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Ile	Thr	Leu	Thr	His	Pro
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Val	Thr	Lys	Tyr	Ile	Met	Thr	Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Val
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Thr	Ser	Thr	Trp	Val	Leu	Val	Gly	Gly	Val	Leu	Ala	Ala	Leu	Ala	Ala

420					425					430					
Tyr	Cys	Leu	Ser	Thr	Gly	Cys	Val	Val	Ile	Val	Gly	Arg	Val	Val	Leu
		435					440					445			
Ser	Gly	Lys	Pro	Ala	Ile	Ile	Pro	Asp	Arg	Glu	Val	Leu	Tyr	Arg	Glu
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Phe	Asp	Glu	Met	Glu	Glu	Cys	Ser	Gln	His	Leu	Pro	Tyr	Ile	Glu	Gln
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Gly	Met	Met	Leu	Ala	Glu	Gln	Phe	Lys	Gln	Lys	Ala	Leu	Gly	Leu	Leu
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Gln	Thr	Ala	Ser	Arg	Gln	Ala	Glu	Val	Ile	Ala	Pro	Ala	Val	Gln	Thr
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Asn	Trp	Gln	Lys	Leu	Glu	Thr	Phe	Trp	Ala	Lys	His	Met	Trp	Asn	Phe
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Ile	Ser	Gly	Ile	Gln	Tyr	Leu	Ala	Gly	Leu	Ser	Thr	Leu	Pro	Gly	Asn
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Pro	Ala	Ile	Ala	Ser	Leu	Met	Ala	Phe	Thr	Ala	Ala	Val	Thr	Ser	Pro
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Leu	Thr	Thr	Ser	Gln	Thr	Leu	Leu	Phe	Asn	Ile	Leu	Gly	Gly	Trp	Val
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Ala	Ala	Gln	Leu	Ala	Ala	Pro	Gly	Ala	Ala	Thr	Ala	Phe	Val	Gly	Ala
			580					585					590		
Gly	Leu	Ala	Gly	Ala	Ala	Ile	Gly	Ser	Val	Gly	Leu	Gly	Lys	Val	Leu
		595					600					605			
Ile	Asp	Ile	Leu	Ala	Gly	Tyr	Gly	Ala	Gly	Val	Ala	Gly	Ala	Leu	Val
	610					615					620				
Ala	Phe	Lys	Ile	Met	Ser	Gly	Glu	Val	Pro	Ser	Thr	Glu	Asp	Leu	Val
625					630					635					640
Asn	Leu	Leu	Pro	Ala	Ile	Leu	Ser	Pro	Gly	Ala	Leu	Val	Val	Gly	Val
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Val	Cys	Ala	Ala	Ile	Leu	Arg	Arg	His	Val	Gly	Pro	Gly	Glu	Gly	Ala
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Val	Gln	Trp	Met	Asn	Arg	Leu	Ile	Ala	Phe	Ala	Ser	Arg	Gly	Asn	His
		675					680					685			
Val	Ser	Pro	Thr	His	Tyr	Val	Pro	Glu	Ser	Asp	Ala	Ala	Ala	Arg	Val
		690				695					700				
Thr	Ala	Ile	Leu	Ser	Ser	Leu	Thr	Val	Thr	Gln	Leu	Leu	Arg	Arg	Leu
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His	Gln	Trp	Ile	Ser	Ser	Glu	Cys	Thr	Thr	Pro	Cys	Ser	Gly	Ser	Trp

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Leu	Arg	Asp	Ile	Trp	Asp	Trp	Ile	Cys	Glu	Val	Leu	Ser	Asp	Phe	Lys				
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Thr	Trp	Leu	Lys	Ala	Lys	Leu	Met	Pro	Gln	Leu	Pro	Gly	Ile	Pro	Phe				
		755					760					765							
Val	Ser	Cys	Gln	Arg	Gly	Tyr	Lys	Gly	Val	Trp	Arg	Gly	Asp	Gly	Ile				
	770					775					780								
Met	His	Thr	Arg	Cys	His	Cys	Gly	Ala	Glu	Ile	Thr	Gly	His	Val	Lys				
785					790					795					800				
Asn	Gly	Thr	Met	Arg	Ile	Val	Gly	Pro	Arg	Thr	Cys	Arg	Asn	Met	Trp				
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Ser	Gly	Thr	Phe	Pro	Ile	Asn	Ala	Tyr	Thr	Thr	Gly	Pro	Cys	Thr	Pro				
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Leu	Pro	Ala	Pro	Asn	Tyr	Thr	Phe	Ala	Leu	Trp	Arg	Val	Ser	Ala	Glu				
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Glu	Tyr	Val	Glu	Ile	Arg	Gln	Val	Gly	Asp	Phe	His	Tyr	Val	Thr	Gly				
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Met	Thr	Thr	Asp	Asn	Leu	Lys	Cys	Pro	Cys	Gln	Val	Pro	Ser	Pro	Glu				
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Phe	Phe	Thr	Glu	Leu	Asp	Gly	Val	Arg	Leu	His	Arg	Phe	Ala	Pro	Pro				
				885				890						895					
Cys	Lys	Pro	Leu	Leu	Arg	Glu	Glu	Val	Ser	Phe	Arg	Val	Gly	Leu	His				
			900					905					910						
Glu	Tyr	Pro	Val	Gly	Ser	Gln	Leu	Pro	Cys	Glu	Pro	Glu	Pro	Asp	Val				
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Ala	Val	Leu	Thr	Ser	Met	Leu	Thr	Asp	Pro	Ser	His	Ile	Thr	Ala	Glu				
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Ala	Ala	Gly	Arg	Arg	Leu	Ala	Arg	Gly	Ser	Pro	Pro	Ser	Val	Ala	Ser				
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Ser	Ser	Ala	Ser	Gln	Leu	Ser	Ala	Pro	Ser	Leu	Lys	Ala	Thr	Cys	Thr				
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Ala	Asn	His	Asp	Ser	Pro	Asp	Ala	Glu	Leu	Ile	Glu	Ala	Asn	Leu	Leu				
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Trp	Arg	Gln	Glu	Met	Gly	Gly	Asn	Ile	Thr	Arg	Val	Glu	Ser	Glu	Asn				
		995					1000					1005							
Lys	Val	Val	Ile	Leu	Asp	Ser	Phe	Asp	Pro	Leu	Val	Ala	Glu	Glu	Asp				
	1010					1015						1020							
Glu	Arg	Glu	Ile	Ser	Val	Pro	Ala	Glu	Ile	Leu	Arg	Lys	Ser	Arg	Arg				

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Phe Ala Gln Ala Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro	1045	1050	1055
Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His	1060	1065	1070
Gly Cys Pro Leu Pro Pro Pro Lys Ser Pro Pro Val Pro Pro Pro Arg	1075	1080	1085
Lys Lys Arg Thr Val Val Leu Thr Glu Ser Thr Leu Ser Thr Ala Leu	1090	1095	1100
Ala Glu Leu Ala Thr Arg Ser Phe Gly Ser Ser Ser Thr Ser Gly Ile	1105	1110	1115
Thr Gly Asp Asn Thr Thr Thr Ser Ser Glu Pro Ala Pro Ser Gly Cys	1125	1130	1135
Pro Pro Asp Ser Asp Ala Glu Ser Tyr Ser Ser Met Pro Pro Leu Glu	1140	1145	1150
Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser Trp Ser Thr Val	1155	1160	1165
Ser Ser Glu Ala Asn Ala Glu Asp Val Val Cys Cys Ser Met Ser Tyr	1170	1175	1180
Ser Trp Thr Gly Ala Leu Val Thr Pro Cys Ala Ala Glu Glu Gln Lys	1185	1190	1195
Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg His His Asn Leu	1205	1210	1215
Val Tyr Ser Thr Thr Ser Arg Ser Ala Cys Gln Arg Gln Lys Lys Val	1220	1225	1230
Thr Phe Asp Arg Leu Gln Val Leu Asp Ser His Tyr Gln Asp Val Leu	1235	1240	1245
Lys Glu Val Lys Ala Ala Ala Ser Lys Val Lys Ala Asn Leu Leu Ser	1250	1255	1260
Val Glu Glu Ala Cys Ser Leu Thr Pro Pro His Ser Ala Lys Ser Lys	1265	1270	1275
Phe Gly Tyr Gly Ala Lys Asp Val Arg Cys His Ala Arg Lys Ala Val	1285	1290	1295
Thr His Ile Asn Ser Val Trp Lys Asp Leu Leu Glu Asp Asn Val Thr	1300	1305	1310
Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val Phe Cys Val Gln	1315	1320	1325
Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile Val Phe Pro Asp			



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Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr Asp Val Val Thr		
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Lys Leu Pro Leu Ala Val Met Gly Ser Ser Tyr Gly Phe Gln Tyr Ser		
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Pro Gly Gln Arg Val Glu Phe Leu Val Gln Ala Trp Lys Ser Lys Lys		
	1380	1385 1390
Thr Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val		
	1395	1400 1405
Thr Glu Ser Asp Ile Arg Thr Glu Glu Ala Ile Tyr Gln Cys Cys Asp		
	1410	1415 1420
Leu Asp Pro Gln Ala Arg Val Ala Ile Lys Ser Leu Thr Glu Arg Leu		
	1425	1430 1435 1440
Tyr Val Gly Gly Pro Leu Thr Asn Ser Arg Gly Glu Asn Cys Gly Tyr		
	1445	1450 1455
Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys Gly Asn Thr		
	1460	1465 1470
Leu Thr Cys Tyr Ile Lys Ala Arg Ala Ala Cys Arg Ala Ala Gly Leu		
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Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val Val Ile Cys		
	1490	1495 1500
Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Leu Arg Ala Phe Thr		
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Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Gln Pro		
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Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser Asn Val Ser Val		
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Ala His Asp Gly Ala Gly Lys Arg Val Tyr Tyr Leu Thr Arg Asp Pro		
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Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala Arg His Thr Pro		
	1570	1575 1580
Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe Ala Pro Thr Leu Trp		
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Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Val Leu Ile Ala Arg		
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Asp Gln Leu Glu Gln Ala Leu Asp Cys Glu Ile Tyr Gly Ala Cys Tyr		
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Ser Ile Glu Pro Leu Asp Leu Pro Pro Ile Ile Gln Arg Leu His Gly		

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Val Ala Ala Cys Leu Arg Lys Leu Gly Val Pro Pro Leu Arg Ala Trp		
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Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu Ala Arg Gly Gly		
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Arg Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn Trp Ala Val Arg Thr		
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Lys Leu Lys Leu Thr Pro Ile Ala Ala Gly Gln Leu Asp Leu Ser		
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Gly Trp Phe Thr Ala Gly Tyr Ser Gly Gly Asp Ile Tyr His Ser Val		
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Ser His Ala Arg Pro Arg Trp Ile Trp Phe Cys Leu Leu Leu Leu Ala		
1745	1750	1755 1760
Ala Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg Met Ser Thr Asn Pro		
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Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp		
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Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu Leu		
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Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser		
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Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg		
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Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu		
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Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro Arg		
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Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser Arg		
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Asn Leu Gly Lys		
1890		

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Gly Ala Lys Gln Asn  
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Pro Ala Ile Ile Pro Lys Lys  
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